

OM protein - protein search, using sw model

Run on: **March 31, 2006**, 13:13:34 ; Search time 44 Seconds
 (without alignments)
 1618.191 Million cell updates/sec

Title: **US-09-743-647A-35**
 Perfect score: 3839
 Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 283416 seqs, 96216763 residues
 Total number of hits satisfying chosen parameters: 283416
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : **PIR_80:***
 1: pir1: *
 2: pir2: *
 3: pir3: *
 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1307	34.0	750	2	A56881	prostate-specific
2	973.5	25.4	751	2	T30154	hypothetical prote
3	903	23.5	1483	2	T19751	hypothetical prote
4	865.5	22.5	703	2	T47631	Peptidase-like pro
5	598	15.6	757	2	A48592	transferrin recept
6	593	15.4	776	1	JH0570	transferrin recept
7	583.5	15.2	760	1	JXHU	transferrin recept
8	559.5	14.6	622	2	A34549	transferrin recept
9	557	14.5	763	1	S29548	transferrin recept
10	528.5	13.8	794	2	T40289	hypothetical prote
11	496.5	12.9	811	2	S57149	probable membrane
12	426	11.1	280	2	E85075	probable peptidase
13	305	7.9	783	2	S65188	secretory protein
14	269	7.0	809	2	S67153	probable membrane
15	211	5.5	466	2	E84132	aminopeptidase BH3
16	191	5.0	467	2	G87564	aminopeptidase, pr
17	186	4.8	529	2	G82759	hypothetical prote
18	185	4.8	455	2	S39663	aminopeptidase hom
19	176	4.6	536	2	B83278	probable aminopept
20	174	4.5	500	2	H70629	probable AMINOPEPT
21	172.5	4.5	840	2	T02164	hypothetical prote

22	172	4.5	430	2	A87634	peptidase, M20/M25
23	165	4.3	805	2	G87662	peptidase, M20/M25
24	158.5	4.1	501	2	C82414	aminopeptidase VCA
25	157.5	4.1	571	2	H87600	hypothetical prote
26	155.5	4.1	504	2	S24314	bacterial leucyl a
27	147.5	3.8	449	2	H97249	protein containing
28	146	3.8	284	2	S66427	aminopeptidase (EC
29	145	3.8	537	2	A54134	aminopeptidase Y (
30	144.5	3.8	488	2	A87569	peptidase M20/M25/
31	142.5	3.7	647	2	A83606	hypothetical prote
32	136.5	3.6	1331	2	A72647	probable surface l
33	131	3.4	468	2	F87359	leucine aminopecti
34	129.5	3.4	493	2	T46974	leucyl aminopectid
35	126	3.3	441	2	A84351	hypothetical prote
36	123.5	3.2	1274	2	E81779	proline dehydrogen
37	123	3.2	886	2	T35469	probable ATP /GTP-
38	122.5	3.2	2297	2	T34918	polyketide synthas
39	122	3.2	1331	2	AE1843	hypothetical prote
40	121.5	3.2	1201	2	F81202	proline dehydrogen
41	118	3.1	433	2	F84215	aminopeptidase [im
42	116.5	3.0	909	2	G69599	aconitate hydratas
43	116	3.0	567	2	C72698	hypothetical prote
44	116	3.0	2175	1	GNNYBE	genome polyprotein
45	116	3.0	4735	2	T17463	rifamycin polyketi

ALIGNMENTS

RESULT 1

A56881

prostate-specific membrane antigen - human

C;Species: Homo sapiens (man)

C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: A56881

R;Israeli, R.S.; Powell, C.T.; Fair, W.R.; Heston, W.D.

Cancer Res. 53, 227-230, 1993

A;Title: Molecular cloning of a complementary DNA encoding a prostate-specific membrane antigen.

A;Reference number: A56881; MUID:93113576; PMID:8417812

A;Accession: A56881

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-750 <ISR>

A;Cross-references: UNIPROT:Q04609; UNIPARC:UPI0000000A01; GB:M99487;

NID:g190663; PIDN:AAA60209.1; PID:g190664

A;Experimental source: prostatic carcinoma cell line LNCaP

A;Note: sequence extracted from NCBI backbone (NCBIN:121724, NCBIP:121725)

C;Superfamily: transferrin receptor

C;Keywords: surface antigen; transmembrane protein

Query Match 34.0%; Score 1307; DB 2; Length 750;

Best Local Similarity 38.8%; Pred. No. 2.2e-84;

Matches 293; Conservative 138; Mismatches 267; Indels 58; Gaps 21;

Qy	12	GAAALLG---- <td>66</td>	66
		: : : : : :	
Db	24	GALVLAGGFFLLGLFLGWFIFKSSNEATNITPK----HNMKAFLEDELKAENIKKFLYNFTQ	79

OM protein - protein search, using sw model

Run on: **March 31, 2006**, 13:10:09 ; Search time 234 Seconds
(without alignments)
2231.158 Million cell updates/sec

Title: **US-09-743-647A-35**
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : **UniProt_05.80:***
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	3838	99.9	740	1	NALDL_HUMAN	Q9uqq1 homo sapien
2	3135.5	81.7	745	1	NALDL_MOUSE	Q7m758 mus musculu
3	3124.5	81.4	745	1	NALDL_RAT	054697 rattus norv
4	1840	47.9	1321	2	Q4RSL1_TETNG	Q4rs11 tetraodon n
5	1321.5	34.4	751	1	FOLH1_PIG	077564 s glutamate
6	1308.5	34.1	738	2	Q5BL58_XENTR	Q5bl58 xenopus tro
7	1307	34.0	745	2	Q7ZUD9_BRARE	Q7zud9 brachydanio
8	1307	34.0	750	1	FOLH1_HUMAN	Q04609 h glutamate
9	1307	34.0	750	2	Q541A4_HUMAN	Q541a4 homo sapien
10	1299	33.8	740	1	NALD2_HUMAN	Q9y3q0 homo sapien
11	1299	33.8	740	2	Q4VAM9_HUMAN	Q4vam9 homo sapien
12	1295.5	33.7	752	1	FOLH1_RAT	P70627 r glutamate
13	1295.5	33.7	752	2	Q547B6_RAT	Q547b6 rattus norv
14	1295	33.7	754	2	Q4KLV0_XENLA	Q4klv0 xenopus lae
15	1278.5	33.3	752	1	FOLH1_MOUSE	035409 m glutamate
16	1277.5	33.3	740	1	NALD2_MOUSE	Q9czz2 mus musculu
17	1200.5	31.3	719	2	Q8TAY3_HUMAN	Q8tay3 homo sapien
18	990	25.8	770	1	GCP2_CAEER	Q5wn23 caenorhabdi
19	976.5	25.4	770	1	GCP2_CAEER	P91406 caenorhabdi
20	973.5	25.4	751	2	Q4Z8H5_CAEER	Q4z8h5 caenorhabdi
21	942.5	24.6	728	2	Q5JKV3_ORYSA	Q5jkv3 oryza sativ
22	936	24.4	681	2	Q7Y228_ARATH	Q7y228 arabidopsis
23	910	23.7	745	2	Q93332_CAEER	Q93332 caenorhabdi

24	896.5	23.4	774	2	Q610T9_CAEBR	Q610t9	caenorhabdi
25	882.5	23.0	705	1	GCP2_ARATH	Q9mls8	arabidopsis
26	863.5	22.5	442	2	Q9HBA9_HUMAN	Q9hba9	homo sapien
27	814.5	21.2	760	2	Q6CQJ7_KLULA	Q6cqj7	kluveromyces
28	804	20.9	772	2	Q852M4_ORYSA	Q852m4	oryza sativ
29	790.5	20.6	884	2	Q5B3F5_EMENI	Q5b3f5	aspergillus
30	773	20.1	907	2	Q4WXT7_ASPFU	Q4wxt7	aspergillus
31	769.5	20.0	790	2	Q7NKV9_GLOVI	Q7nkv9	gloeobacter
32	769	20.0	758	2	Q6CFP0_YARLI	Q6cfp0	yarrowia li
33	766	20.0	925	2	Q7SAE5_NEUCR	Q7sae5	neurospora
34	762	19.8	810	2	Q7SFY6_NEUCR	Q7sfy6	neurospora
35	754	19.6	866	2	Q4PCE6_USTMA	Q4pce6	ustilago ma
36	748.5	19.5	772	2	Q5B612_EMENI	Q5b612	aspergillus
37	742.5	19.3	661	2	Q5JNK6_ORYSA	Q5jnk6	oryza sativ
38	742	19.3	727	2	Q52GB6_MAGGR	Q52gb6	magnaporthe
39	733	19.1	705	2	Q70U68_PHYPO	Q70u68	physarum po
40	731	19.0	942	2	Q560F9_CRYNE	Q560f9	cryptococcus
41	730.5	19.0	745	2	Q51JT1_MAGGR	Q51jt1	magnaporthe
42	727.5	19.0	706	2	Q6J516_PHYPO	Q6j516	physarum po
43	727.5	19.0	724	2	Q4I3R7_GIBZE	Q4i3r7	gibberella
44	722.5	18.8	717	2	Q4II44_GIBZE	Q4ii44	gibberella
45	722.5	18.8	911	2	Q5KPG1_CRYNE	Q5kpg1	cryptococcus

ALIGNMENTS

RESULT 1

NALDL_HUMAN

ID NALDL_HUMAN STANDARD; PRT; 740 AA.
AC Q9UQQ1; O43176;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE **N-acetylated-alpha-linked acidic dipeptidase-like protein**
DE (EC 3.4.17.21) (**NAALADase L**) (Ileal dipeptidylpeptidase) (100 kDa
DE ileum brush border membrane protein) (I100).
GN Name=NAALADL1; Synonyms=NAALADASEL, NAALADL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
RC TISSUE=Small intestine;
RX MEDLINE=99185063; PubMed=10085079; DOI=10.1074/jbc.274.13.8470;
RA **Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,**
RA **van der Helm L., Fraiponts E., Ashton D., Gordon R.D.;**
RT **"Isolation and expression of novel human glutamate carboxypeptidases**
RT **with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl**
RT **peptidase IV activity.";**
RL **J. Biol. Chem. 274:8470-8483(1999).**
RN [2]
RP NUCLEOTIDE SEQUENCE OF 419-740.
RC TISSUE=Ileum;
RX MEDLINE=98049571; PubMed=9388249; DOI=10.1074/jbc.272.49.31006;
RA **Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Rinaldo P.,**
RA **Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.;**

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OM protein - protein search, using sw model

Run on: **March 31, 2006**, 13:09:39 ; Search time 192 Seconds
(without alignments)
1693.439 Million cell updates/sec

Title: **US-09-743-647A-35**
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : **A_Geneseq_21.***
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3839	100.0	745	4 ABG09829	Abg09829 Novel hum
2	3838	99.9	740	3 AAY58870	Aay58870 Human pep
3	3838	99.9	740	9 ADZ97838	Adz97838 Human NAA
4	3608.5	94.0	705	3 AAY58873	Aay58873 Human pep
5	3603.5	93.9	705	3 AAY58872	Aay58872 Human pep
6	3600.5	93.8	699	3 AAY58871	Aay58871 Human pep
7	3313.5	86.3	687	8 ADI16329	Adi16329 Human pro
8	3226	84.0	635	3 AAY58877	Aay58877 Human pep
9	2947	76.8	578	3 AAY58876	Aay58876 Human pep
10	2637.5	68.7	522	3 AAY58875	Aay58875 Human pep
11	2633.5	68.6	544	3 AAY58874	Aay58874 Human pep
12	1324	34.5	750	3 AAY92640	Aay92640 Mutant hu
13	1309	34.1	750	3 AAB44334	Aab44334 Human PRO
14	1309	34.1	750	4 AAU29075	Aau29075 Human PRO
15	1309	34.1	750	6 ABU58451	Abu58451 Human PRO

16	1309	34.1	750	6	ABU87999	Abu87999	Novel	hum
17	1309	34.1	750	6	ABU84314	Abu84314	Human	sec
18	1309	34.1	750	6	ABR66188	Abr66188	Human	sec
19	1309	34.1	750	6	ABR65578	Abr65578	Human	sec
20	1309	34.1	750	6	ABU99518	Abu99518	Human	sec
21	1309	34.1	750	6	ABU82757	Abu82757	Human	PRO
22	1309	34.1	750	6	ABU89878	Abu89878	Novel	hum
23	1309	34.1	750	6	ABR68127	Abr68127	Human	sec
24	1309	34.1	750	6	ABU96180	Abu96180	Novel	hum
25	1309	34.1	750	6	ABU92611	Abu92611	Human	sec
26	1309	34.1	750	6	ABO08688	Abo08688	Human	sec
27	1309	34.1	750	6	ABO02740	Abo02740	Human	sec
28	1309	34.1	750	6	ABR74894	Abr74894	Human	sec
29	1309	34.1	750	6	ABR94656	Abr94656	Human	sec
30	1309	34.1	750	6	ABO25280	Abo25280	Novel	hum
31	1309	34.1	750	6	ABU85629	Abu85629	Human	PRO
32	1309	34.1	750	6	ABU98789	Abu98789	Novel	hum
33	1309	34.1	750	6	ABU98004	Abu98004	Novel	hum
34	1309	34.1	750	6	ABU91710	Abu91710	Novel	hum
35	1309	34.1	750	6	ABU72286	Abu72286	Novel	hum
36	1309	34.1	750	6	ABU89403	Abu89403	Human	PRO
37	1309	34.1	750	6	ABU86244	Abu86244	Human	sec
38	1309	34.1	750	6	ABU67457	Abu67457	Human	sec
39	1309	34.1	750	6	ABU80485	Abu80485	Human	PRO
40	1309	34.1	750	6	ABR99403	Abr99403	Human	sec
41	1309	34.1	750	6	ABR98793	Abr98793	Human	sec
42	1309	34.1	750	6	ABO16316	Abo16316	Human	sec
43	1309	34.1	750	6	ABR92216	Abr92216	Human	sec
44	1309	34.1	750	6	ABO18857	Abo18857	Human	sec
45	1309	34.1	750	6	ABR78278	Abr78278	Human	sec

ALIGNMENTS

RESULT 1

ABG09829

ID ABG09829 standard; protein; 745 AA.
AC ABG09829;
DT 13-FEB-2002 (first entry)
DE Novel human diagnostic protein #9820.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
OS Homo sapiens.
PN WO200175067-A2.
PD 11-OCT-2001.
PF 30-MAR-2001; 2001WO-US008631.
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
DR WPI; 2001-639362/73.
DR N-PSDB; AAS74016.
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
PS Claim 20; SEQ ID NO 40188; 103pp; English.

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OM protein - nucleic search, using frame_plus_p2n model
Run on: **March 31, 2006**, 17:07:00 ; Search time 345 Seconds
(without alignments)
3812.741 Million cell updates/sec

Title: **US-09-743-647A-35**
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09743647/runat_31032006_094835_15847/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss07 -USER=US09743647_@CGN_1_1_193_@runat_31032006_094835_15847
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : **Issued_Patents_NA:***
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID		Description
1	1309	34.1	2558	3	US-09-999-833A-617		Sequence 617, App

2	1309	34.1	2558	3	US-10-020-445A-617	Sequence 617, App
3	1307	34.0	2653	2	US-08-325-553-1	Sequence 1, Appli
4	1307	34.0	2653	2	US-08-394-152A-1	Sequence 1, Appli
5	1307	34.0	2653	3	US-08-705-477E-1	Sequence 1, Appli
6	1307	34.0	2653	3	US-09-973-382C-3	Sequence 3, Appli
7	1307	34.0	2653	3	US-08-466-381C-1	Sequence 1, Appli
8	1293.5	33.7	2133	3	US-09-164-034B-1	GENERAL INFORMA
9	1282.5	33.4	2387	3	US-08-705-477E-100	Sequence 100, App
10	1040	27.1	1992	3	US-09-973-382C-1	Sequence 1, Appli
11	709	18.5	2877	3	US-09-358-755-2	Sequence 2, Appli
12	705	18.4	2519	3	US-09-358-755-3	Sequence 3, Appli
13	645.5	16.8	2513	3	US-09-949-016-1366	Sequence 1366, Ap
14	593.5	15.5	2826	3	US-09-023-655-1324	Sequence 1324, Ap
15	593.5	15.5	4080	3	US-09-016-434-1352	Sequence 1352, Ap
16	593.5	15.5	5010	3	US-09-161-244-1	Sequence 1, Appli
17	578.5	15.1	8731	3	US-09-919-039-350	Sequence 350, App
18	391.5	10.2	915	3	US-09-248-796A-6742	Sequence 6742, Ap
19	318	8.3	780	2	US-08-325-553-27	Sequence 27, Appl
20	318	8.3	780	2	US-08-394-152A-27	Sequence 27, Appl
21	318	8.3	780	3	US-08-705-477E-27	Sequence 27, Appl
22	318	8.3	780	3	US-08-466-381C-27	Sequence 27, Appl
23	305	7.9	2352	3	US-09-614-221A-77	Sequence 77, Appl
24	284	7.4	1185	3	US-09-248-796A-6116	Sequence 6116, Ap
25	274	7.1	624	3	US-09-533-559-747	Sequence 747, App
26	265	6.9	540	2	US-08-325-553-29	Sequence 29, Appl
27	265	6.9	540	2	US-08-394-152A-29	Sequence 29, Appl
28	265	6.9	540	3	US-08-705-477E-29	Sequence 29, Appl
29	265	6.9	540	3	US-08-466-381C-29	Sequence 29, Appl
30	226	5.9	660	2	US-08-325-553-28	Sequence 28, Appl
31	226	5.9	660	2	US-08-394-152A-28	Sequence 28, Appl
32	226	5.9	660	3	US-08-705-477E-28	Sequence 28, Appl
33	226	5.9	660	3	US-08-466-381C-28	Sequence 28, Appl
c 34	222.5	5.8	11358	3	US-09-902-540-1075	Sequence 1075, Ap
35	220.5	5.7	1317	3	US-09-902-540-9439	Sequence 9439, Ap
36	220.5	5.7	1584	3	US-09-248-796A-6743	Sequence 6743, Ap
c 37	216.5	5.6	231	3	US-09-439-313-454	Sequence 454, App
c 38	216.5	5.6	231	3	US-09-352-616A-454	Sequence 454, App
c 39	216.5	5.6	231	3	US-09-636-215-454	Sequence 454, App
c 40	216.5	5.6	231	3	US-09-685-166A-454	Sequence 454, App
c 41	216.5	5.6	231	3	US-09-679-426-454	Sequence 454, App
c 42	216.5	5.6	231	3	US-09-759-143-454	Sequence 454, App
c 43	216.5	5.6	231	3	US-09-651-236-454	Sequence 454, App
c 44	216.5	5.6	231	3	US-09-657-279-454	Sequence 454, App
c 45	216.5	5.6	231	3	US-10-012-896-454	Sequence 454, App

ALIGNMENTS

RESULT 1

US-09-999-833A-617

; **Sequence 617**, Application US/09999833A

; Patent No. **6916648**

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

OM protein - protein search, using sw model
 Run on: **March 31, 2006**, 13:28:40 ; Search time 167 Seconds
 (without alignments)
 1851.459 Million cell updates/sec

Title: **US-09-743-647A-35**
 Perfect score: 3839
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 1867569 seqs, 417829326 residues
 Total number of hits satisfying chosen parameters: 1867569
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1309	34.1	750	3	US-09-978-295A-618	Sequence 618, App
3	1309	34.1	750	3	US-09-978-697-618	Sequence 618, App
4	1309	34.1	750	3	US-09-978-192A-618	Sequence 618, App
5	1309	34.1	750	3	US-09-999-832A-618	Sequence 618, App
6	1309	34.1	750	3	US-09-978-189-618	Sequence 618, App
7	1309	34.1	750	3	US-09-978-608A-618	Sequence 618, App
8	1309	34.1	750	3	US-09-978-585A-618	Sequence 618, App
9	1309	34.1	750	3	US-09-978-191A-618	Sequence 618, App
10	1309	34.1	750	3	US-09-978-403A-618	Sequence 618, App
11	1309	34.1	750	3	US-09-978-564A-618	Sequence 618, App
12	1309	34.1	750	3	US-09-999-833A-618	Sequence 618, App
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14	1309	34.1	750	3	US-09-978-824-618	Sequence 618, App
15	1309	34.1	750	3	US-09-918-585A-618	Sequence 618, App
16	1309	34.1	750	3	US-09-999-834A-618	Sequence 618, App
17	1309	34.1	750	3	US-09-978-423A-618	Sequence 618, App
18	1309	34.1	750	3	US-09-978-193A-618	Sequence 618, App
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20	1309	34.1	750	3	US-09-978-757A-618	Sequence 618, App
21	1309	34.1	750	3	US-09-978-187B-618	Sequence 618, App
22	1309	34.1	750	3	US-09-978-643A-618	Sequence 618, App
23	1309	34.1	750	3	US-09-978-375A-618	Sequence 618, App
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28	1309	34.1	750	3	US-09-999-829A-618	Sequence 618, App
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37	1309	34.1	750	4	US-10-176-758-104	Sequence 104, App
38	1309	34.1	750	4	US-10-175-737-104	Sequence 104, App
39	1309	34.1	750	4	US-10-174-581-104	Sequence 104, App
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ALIGNMENTS

RESULT 1

US-10-450-763-40188

; Sequence 40188, Application US/10450763

; Publication No. **US20050196754A1**

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: **US/10/450,763**

; CURRENT FILING DATE: **2003-06-11**

; PRIOR APPLICATION NUMBER: **PCT/US01/08631**

; PRIOR FILING DATE: **2001-03-30**

; PRIOR APPLICATION NUMBER: **09/540,217**

; PRIOR FILING DATE: **2000-03-31**

; PRIOR APPLICATION NUMBER: **09/649,167**

; PRIOR FILING DATE: **2000-08-23**

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 40188

; LENGTH: 745

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: DOMAIN LOCATION: (167)..(259)

; OTHER INFORMATION: PA domain identified by PFam, accession name PA, E-value=5.8e

; OTHER INFORMATION: -21, PFam score of 83.1

US-10-450-763-40188

Query Match 100.0%; Score 3839; DB 5; Length 745;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: **March 31, 2006**, 13:29:45 ; Search time 26 Seconds
(without alignments)
866.423 Million cell updates/sec

Title: **US-09-743-647A-35**
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 180808 seqs, 30441898 residues
Total number of hits satisfying chosen parameters: 180808
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1307	34.0	750	7	US-11-073-347-1	Sequence 1, Appli
2	1307	34.0	750	7	US-11-155-288-4	Sequence 4, Appli
3	1307	34.0	750	7	US-11-202-516-2	Sequence 2, Appli
4	1294.5	33.7	752	7	US-11-202-516-8	Sequence 8, Appli
5	1276.5	33.3	694	7	US-11-202-516-10	Sequence 10, Appl
6	709	18.5	801	6	US-10-453-372-466	Sequence 466, App
7	705	18.4	801	6	US-10-453-372-468	Sequence 468, App
8	583.5	15.2	760	6	US-10-912-580-4	Sequence 4, Appli
9	583.5	15.2	760	6	US-10-912-585-1	Sequence 1, Appli
10	561.5	14.6	804	6	US-10-912-580-5	Sequence 5, Appli
11	561.5	14.6	804	6	US-10-912-585-2	Sequence 2, Appli
12	391	10.2	489	6	US-10-453-372-460	Sequence 460, App
13	248.5	6.5	424	6	US-10-453-372-458	Sequence 458, App
14	135.5	3.5	1171	6	US-10-467-657-7842	Sequence 7842, Ap
15	116.5	3.0	909	7	US-11-077-619-8	Sequence 8, Appli
16	114.5	3.0	1140	6	US-10-858-730-208	Sequence 208, App
17	113.5	3.0	2523	7	US-11-052-554A-143	Sequence 143, App

18	108	2.8	2399	7	US-11-052-554A-92	Sequence 92, Appl
19	107.5	2.8	462	7	US-11-087-099-3504	Sequence 3504, Ap
20	107.5	2.8	462	7	US-11-087-099-11772	Sequence 11772, A
21	106.5	2.8	565	7	US-11-096-568A-1994	Sequence 1994, Ap
22	106.5	2.8	565	7	US-11-096-568A-27236	Sequence 27236, A
23	106.5	2.8	624	7	US-11-096-568A-1993	Sequence 1993, Ap
24	106.5	2.8	624	7	US-11-096-568A-27235	Sequence 27235, A
25	106.5	2.8	625	7	US-11-096-568A-1992	Sequence 1992, Ap
26	106.5	2.8	625	7	US-11-096-568A-27234	Sequence 27234, A
27	106	2.8	943	6	US-10-467-657-5508	Sequence 5508, Ap
28	104.5	2.7	797	7	US-11-090-617-554	Sequence 554, App
29	103.5	2.7	791	6	US-10-821-234-962	Sequence 962, App
30	103	2.7	1158	6	US-10-858-730-70	Sequence 70, Appl
31	102.5	2.7	878	6	US-10-954-468-41	Sequence 41, Appl
32	101	2.6	1234	6	US-10-995-561-870	Sequence 870, App
33	101	2.6	1365	6	US-10-995-561-867	Sequence 867, App
34	101	2.6	1366	6	US-10-995-561-868	Sequence 868, App
35	101	2.6	1411	6	US-10-995-561-869	Sequence 869, App
36	99.5	2.6	1047	7	US-11-067-260-16	Sequence 16, Appl
37	99.5	2.6	1082	7	US-11-067-260-15	Sequence 15, Appl
38	99.5	2.6	1263	7	US-11-076-163-3	Sequence 3, Appli
39	99.5	2.6	1312	7	US-11-067-260-20	Sequence 20, Appl
40	99.5	2.6	1312	7	US-11-067-260-32	Sequence 32, Appl
41	99.5	2.6	1389	7	US-11-067-260-52	Sequence 52, Appl
42	99.5	2.6	1392	7	US-11-067-260-24	Sequence 24, Appl
43	99.5	2.6	1403	7	US-11-067-260-58	Sequence 58, Appl
44	99.5	2.6	1444	7	US-11-067-260-46	Sequence 46, Appl
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ALIGNMENTS

RESULT 1

US-11-073-347-1

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; Sequence 1, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; APPLICANT: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR CANCER
; FILE REFERENCE: MANNK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-1
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